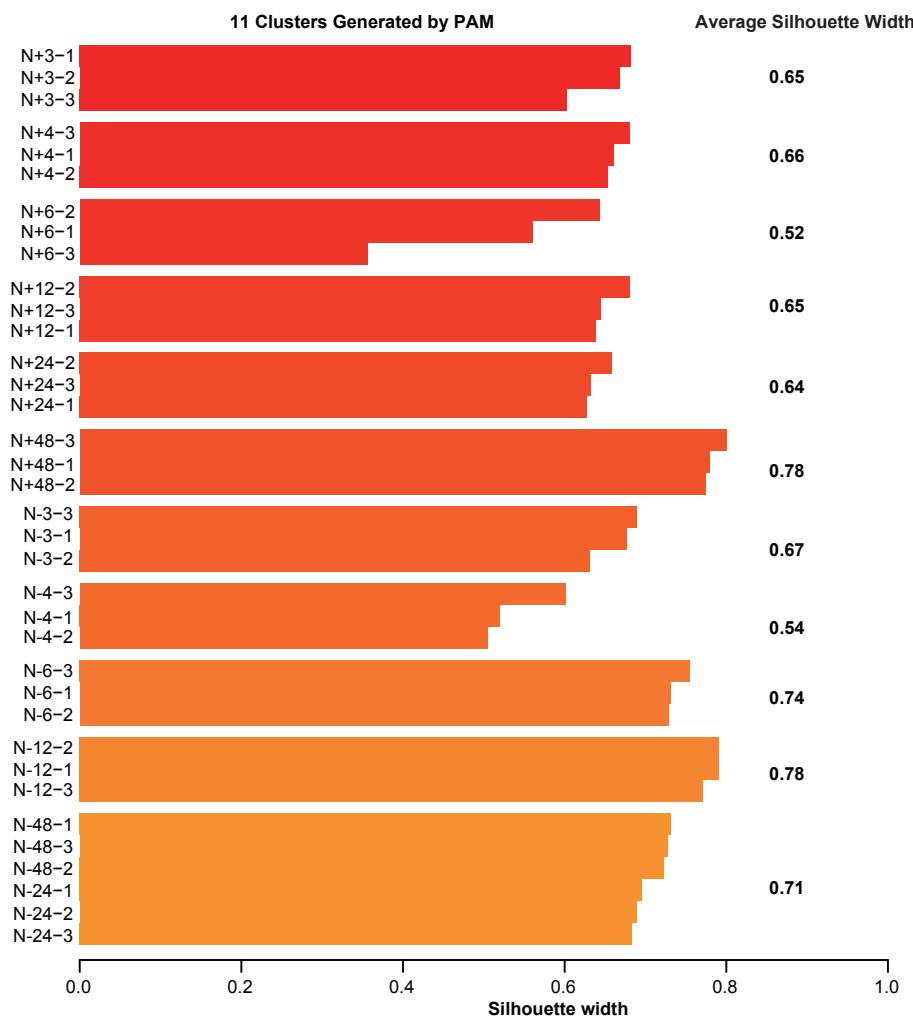
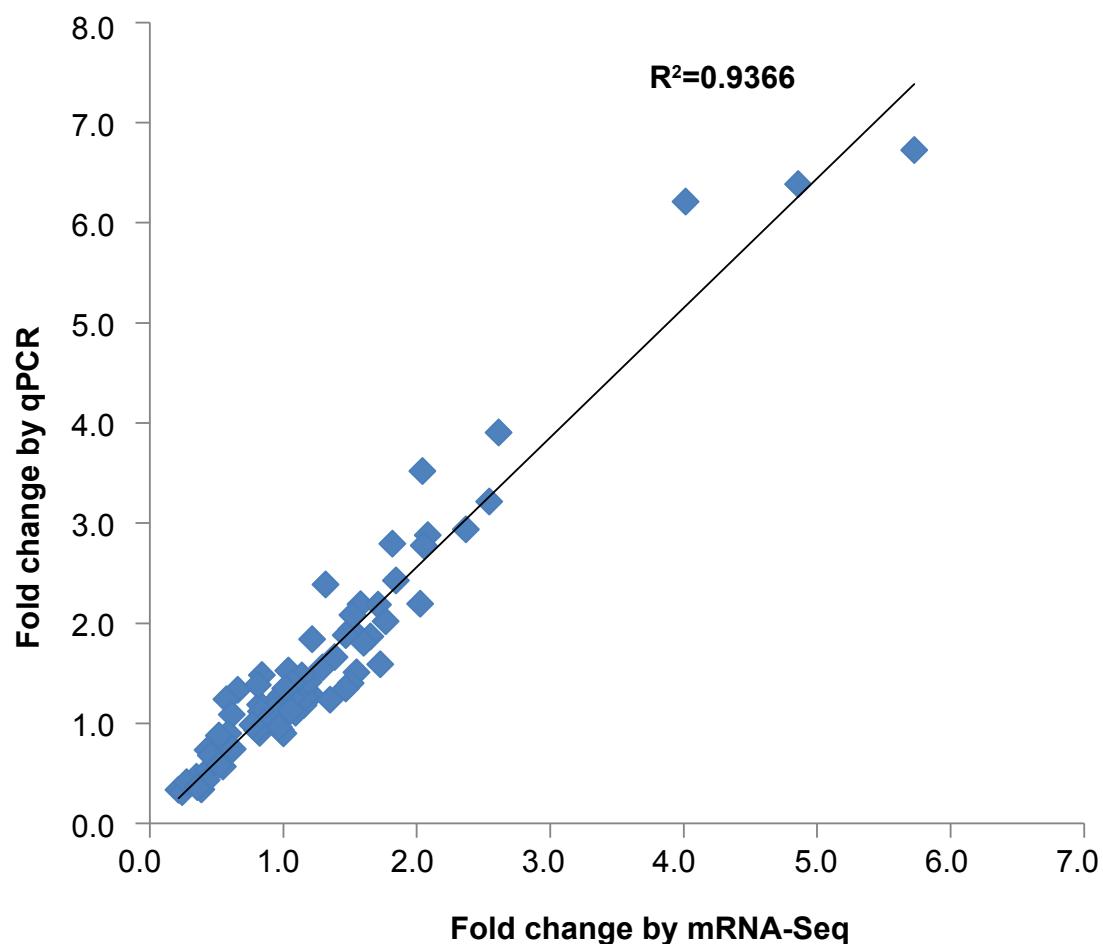


Supplemental Figure 1. Growth curves of IMET1 cells under N+ and N- conditions. Values represent means \pm SD (n=3).



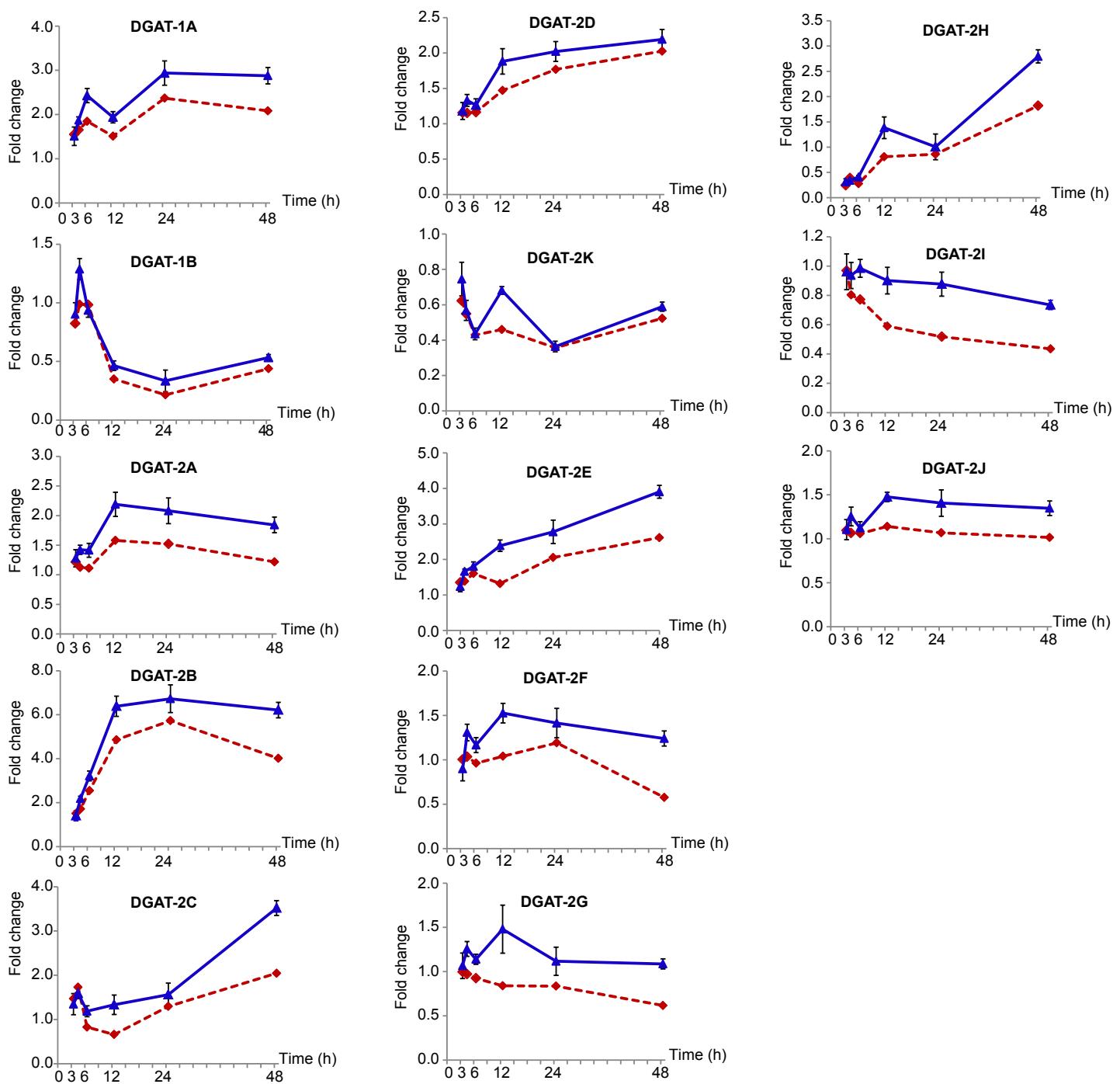
Supplemental Figure 2. Clustering analysis of the mRNA-Seq-based time-series transcriptome dataset. Results from PAM clustering analysis of the 36 transcript profiles are shown. Silhouette plot was applied in this analysis. The average silhouette width of each cluster (indicated by different colors) is presented. The average silhouette width of the 11 clusters is 0.67.



Supplemental Figure 3. Consistency between mRNA-Seq-based and real-time PCR (qPCR)-based transcript quantification. Thirteen genes involved in lipid metabolism were selected for qPCR validation. The genes and qPCR primer sequences are listed in **Supplemental Table 2**. The transcript levels at each time point after the onset of N deprivation are included, and the coefficient of determination between the average qPCR-based transcript abundance and the mRNA-Seq-based transcript abundance is 0.9366 (R^2).

mRNA-Seq

qPCR



Supplemental Figure 4. Transcript abundance and dynamics of the DGAT genes in IMET1 as measured by mRNA-Seq and real-time quantitative PCR. Each data point represents the average of three biological replicates. Each sample was analyzed in technical triplicates. Values represent means \pm SD ($n=3$).

Supplemental Table 1. General information of the mRNA-Seq data.

| Sample | Clean PE reads | Clean reads | Uniquely aligned reads | Aligned ratio | Aligned genes |
|--------|----------------|-------------|------------------------|---------------|---------------|
| N+3-1 | 8,979,962 | 17,959,924 | 15,228,992 | 84.8% | 9,475 |
| N+3-2 | 12,885,355 | 25,770,710 | 21,889,585 | 84.9% | 9,459 |
| N+3-3 | 11,784,442 | 23,568,884 | 20,050,088 | 85.1% | 9,491 |
| N-3-1 | 8,594,898 | 17,189,796 | 14,711,647 | 85.6% | 9,497 |
| N-3-2 | 8,291,151 | 16,582,302 | 14,093,034 | 85.0% | 9,523 |
| N-3-3 | 11,809,533 | 23,619,066 | 20,077,445 | 85.0% | 9,512 |
| N+4-1 | 10,018,733 | 20,037,466 | 17,210,597 | 85.9% | 9,503 |
| N+4-2 | 9,881,875 | 19,763,750 | 17,019,954 | 86.1% | 9,487 |
| N+4-3 | 10,408,021 | 20,816,042 | 17,916,818 | 86.1% | 9,503 |
| N-4-1 | 8,418,644 | 16,837,288 | 14,511,320 | 86.2% | 9,543 |
| N-4-2 | 11,832,807 | 23,665,614 | 20,303,725 | 85.8% | 9,494 |
| N-4-3 | 10,321,528 | 20,643,056 | 17,604,205 | 85.3% | 9,518 |
| N+6-1 | 10,377,352 | 20,754,704 | 17,209,045 | 82.9% | 9,542 |
| N+6-2 | 8,530,339 | 17,060,678 | 14,014,368 | 82.1% | 9,527 |
| N+6-3 | 9,629,621 | 19,259,242 | 16,006,732 | 83.1% | 9,527 |
| N-6-1 | 7,449,602 | 14,899,204 | 12,331,318 | 82.8% | 9,566 |
| N-6-2 | 9,165,757 | 18,331,514 | 15,221,008 | 83.0% | 9,560 |
| N-6-3 | 8,953,202 | 17,906,404 | 14,872,807 | 83.1% | 9,557 |
| N+12-1 | 10,109,427 | 20,218,854 | 16,979,164 | 84.0% | 9,551 |
| N+12-2 | 9,978,426 | 19,956,852 | 16,721,356 | 83.8% | 9,553 |
| N+12-3 | 8,411,678 | 16,823,356 | 14,084,538 | 83.7% | 9,543 |
| N-12-1 | 10,051,881 | 20,103,762 | 16,839,196 | 83.8% | 9,586 |
| N-12-2 | 10,264,329 | 20,528,658 | 17,260,122 | 84.1% | 9,587 |
| N-12-3 | 14,960,251 | 29,920,502 | 26,115,387 | 87.3% | 9,582 |
| N+24-1 | 26,707,658 | 53,415,316 | 44,282,663 | 82.9% | 9,550 |
| N+24-2 | 14,916,284 | 29,832,568 | 25,344,268 | 85.0% | 9,546 |
| N+24-3 | 9,999,944 | 19,999,888 | 16,953,792 | 84.8% | 9,558 |
| N-24-1 | 14,328,166 | 28,656,332 | 23,635,946 | 82.5% | 9,555 |
| N-24-2 | 12,663,572 | 25,327,144 | 21,230,264 | 83.8% | 9,572 |

| | | | | | |
|---------------|------------|------------|------------|-------|-------|
| N-24-3 | 9,721,112 | 19,442,224 | 16,644,614 | 85.6% | 9,551 |
| N+48-1 | 9,795,810 | 19,591,620 | 16,135,798 | 82.4% | 9,555 |
| N+48-2 | 10,370,100 | 20,740,200 | 16,992,181 | 81.9% | 9,538 |
| N+48-3 | 10,035,863 | 20,071,726 | 16,489,828 | 82.2% | 9,566 |
| N-48-1 | 8,660,921 | 17,321,842 | 14,387,470 | 83.1% | 9,563 |
| N-48-2 | 8,618,263 | 17,236,526 | 14,269,436 | 82.8% | 9,553 |
| N-48-3 | 10,397,680 | 20,795,360 | 17,371,266 | 83.5% | 9,544 |

Supplemental Table 2. Real-time PCR primer sequences for the 13 genes used in real-time PCR experiments to validate the mRNA-Seq results.

| Gene name | Gene ID | Forward primer | Reverse primer |
|----------------|-----------------|----------------------------|------------------------------|
| Actin | s00082.g3056 | 5'GCCGTTATTGGATGGATATG3' | 5'ACAAACAACCTCCCTTCACA3' |
| DGAT-1A | iso00738.DGAT1A | 5'ATTGGCGAACCTTCCAATG3' | 5'TGGTCCGTAAGGTAGATG3' |
| DGAT-1B | s00271.g7935 | 5'GATTACTGGCGTCTATGGAA3' | 5'GTAGGCTTGGATGGTGTAA3' |
| DGAT-2A | s00095.g3356 | 5'CAGCAAACGTCAATGTGG3' | 5'TAGTAAAGCTCCTCGACCTT3' |
| DGAT-2B | s00247.g6725 | 5'TTATTGAAATGTGGTGTATTGC3' | 5'CTGACAGAAGAGACTATGGT3' |
| DGAT-2C | s00328.g9146 | 5'GACCTACCTGGACACAAG3' | 5'CTGCGAACAGATGAATTGCT3' |
| DGAT-2D | s00043.g1722 | 5'ATATCCGTATGTTCAAGGT3' | 5'GAAGCCGTAGGTGAAGAG3' |
| DGAT-2E | s00259.g7358 | 5'CTTCGCAACGGATATGAC3' | 5'TGAGCCAACAGCAATAAC3' |
| DGAT-2F | s00354.g10167 | 5'ATTGCTATTGGCTATCTGTT3' | 5'AATCTATCGGGTTACCTACG3' |
| DGAT-2G | s00252.g7156 | 5'GGAGATGTTGGTGGAGAG3' | 5'GTAGTAGTAGTTGTCGTAGCA3' |
| DGAT-2H | s00247.g6698 | 5'CTCGCTTCGCTAACCAT3' | 5'GCCTGCTCTATTGATGTTG3' |
| DGAT-2I | s00043.g2042 | 5'TTGAAGAACCGTGTGGATAT3' | 5'CCGAGAACATCTGACCTTA3' |
| DGAT-2J | s00007.g237 | 5'GCATAAGCAAGGCAGATAA3' | 5'TCATAGAACAGACAGTAGGAGATT3' |
| DGAT-2K | s00330.g9393 | 5'GGCTGTTCAAGTGAGTATCT3' | 5'CCATTGTTAAACCCCTTCC3' |